

SERINE PROTEASE PRIMERS

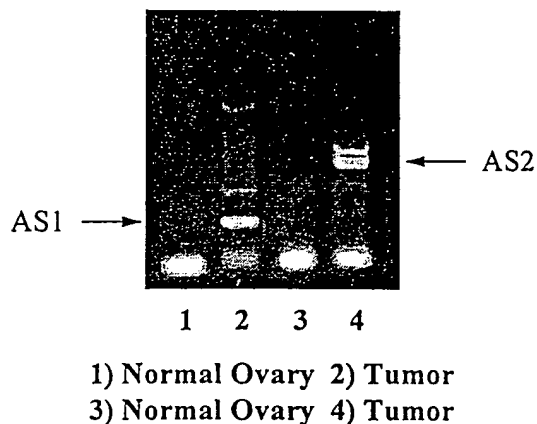


Figure 1 shows a comparison of PCR products derived from normal and carcinoma cDNA as shown by staining in an agarose gel. Two distinct bands (lane 2) were present in the primer pair sense-His-antisense ASP-(AS1) and multiple bands of about 500 bp are noted in the carcinoma lane for the sense-His antisense-SER (AS2) primer pairs (lane 4).

201	Prom	WVLTAAHCKK	PNLQV....F	LGKHNLRQRE	SSQEQSSVVR	AVIHPDY...	SEQ 10 No:1
	Tadg14	WVVTAAHCKK	PKYTV....R	LGDHSLQNKD	GPEQEIPVVQ	SIPHPCY...	SEQ 10 No:2
	Try1	WVVSAGHCYK	SRIQV....R	LGEHNIEVLE	GNEQFINAAK	IIRHPQY...	SEQ 10 No:3
	Scce	WVLTAAHCKM	NEYTV....H	LGSDTLGDRR	A..QRIKASK	SFRHPGY...	SEQ 10 No:4
	Heps	WVLTAAHCFP	ERNRVLSRWR	VFAGAVAQAS	PHGLQLGVQA	VVYHGGYLPF	SEQ 10 No:5
251	Prom	...DAASHDQ	DIMLLRLARP	AKLSELIQPL	PLERDCSA..	NTTSCHILGW	
	Tadg14	NSSDVEDHNH	DLMLIQLRDQ	ASLGSKVKPI	SLADHCTQ..	PGQNCTVSGW	
	Try1	...DRKTLNN	DIMLIKLSR	AVINARVSTI	SLPTAPPA..	TGKCLISGW	
	Scce	ST...QTHVN	DLMLVKLNSQ	ARLSSMVKKV	RLPSRCEP..	PGTTCTVSGW	
	Heps	RDPNSEENSN	DIALVHLSSP	LPLTEYIQPV	CLPAAGQALV	DGKICTVTGW	
301	Prom	GKTAD..GDF	PDTIQCAYIH	LVSREECEHA	..YPGQITQN	MLCAGDEKYG	
	Tadg14	GTVTSPRENF	PDTLNCAEVK	IFPQKKCEDA	..YPGQITDG	MVCAGSSK.G	
	Try1	GNTASSGADY	PDELQCLDAP	VLSQAKCEAS	..YPGKITSN	MFCVGFLEGG	
	Scce	GTTTSPDVTF	PSDLMCVDVK	LISPQDCTKV	..YKDLENS	MLCAGIPDSK	
	Heps	GNTQYYGQQ.	AGVLQEARVP	IISNDVCNGA	DFYGNQIKPK	MFCAGYPEGG	
351	Prom	KDSCGDSGG					
	Tadg14	ADTCGDSGG					
	Try1	KDSCGDSGG					
	Scce	KNACMGDSGG					
	Heps	IDACGDSGG					

Figure 2. Comparison of amino acid sequence of TADG-14 with known serine protease catalytic domains.

OVER EXPRESSION OF TADG 14

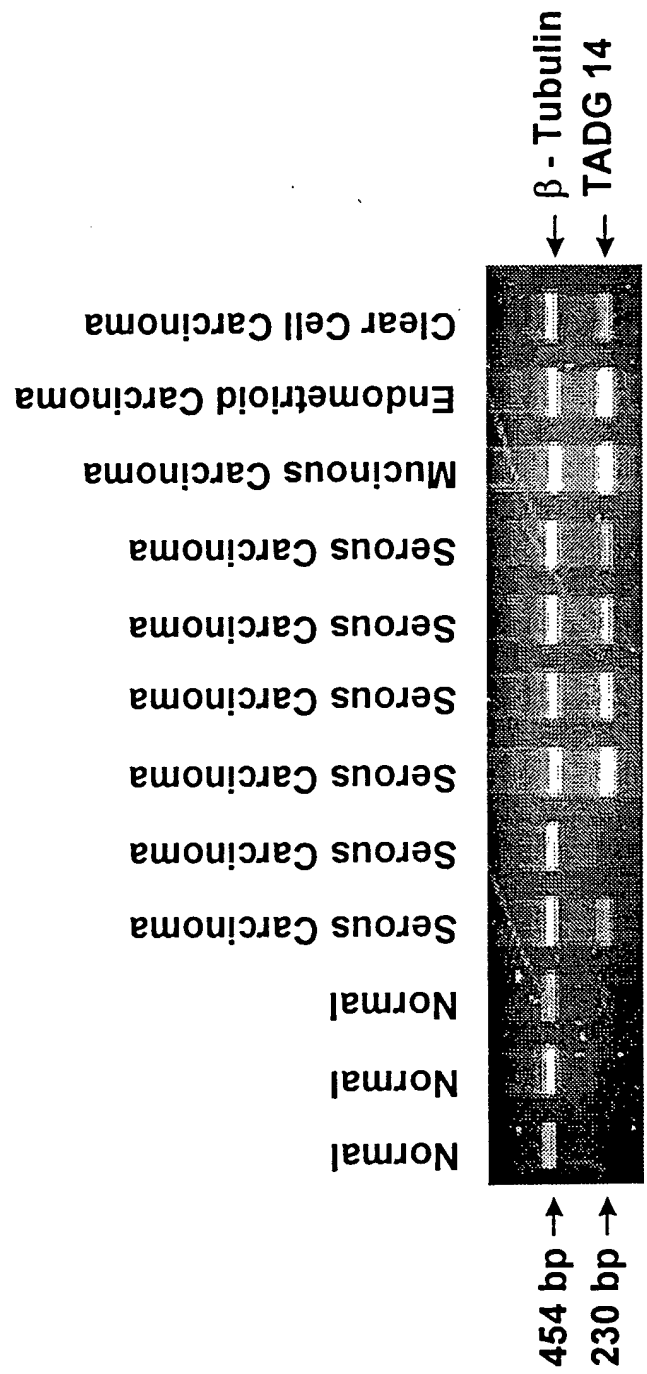


Figure 3. Overexpression of TADG-14 in ovarian carcinomas.

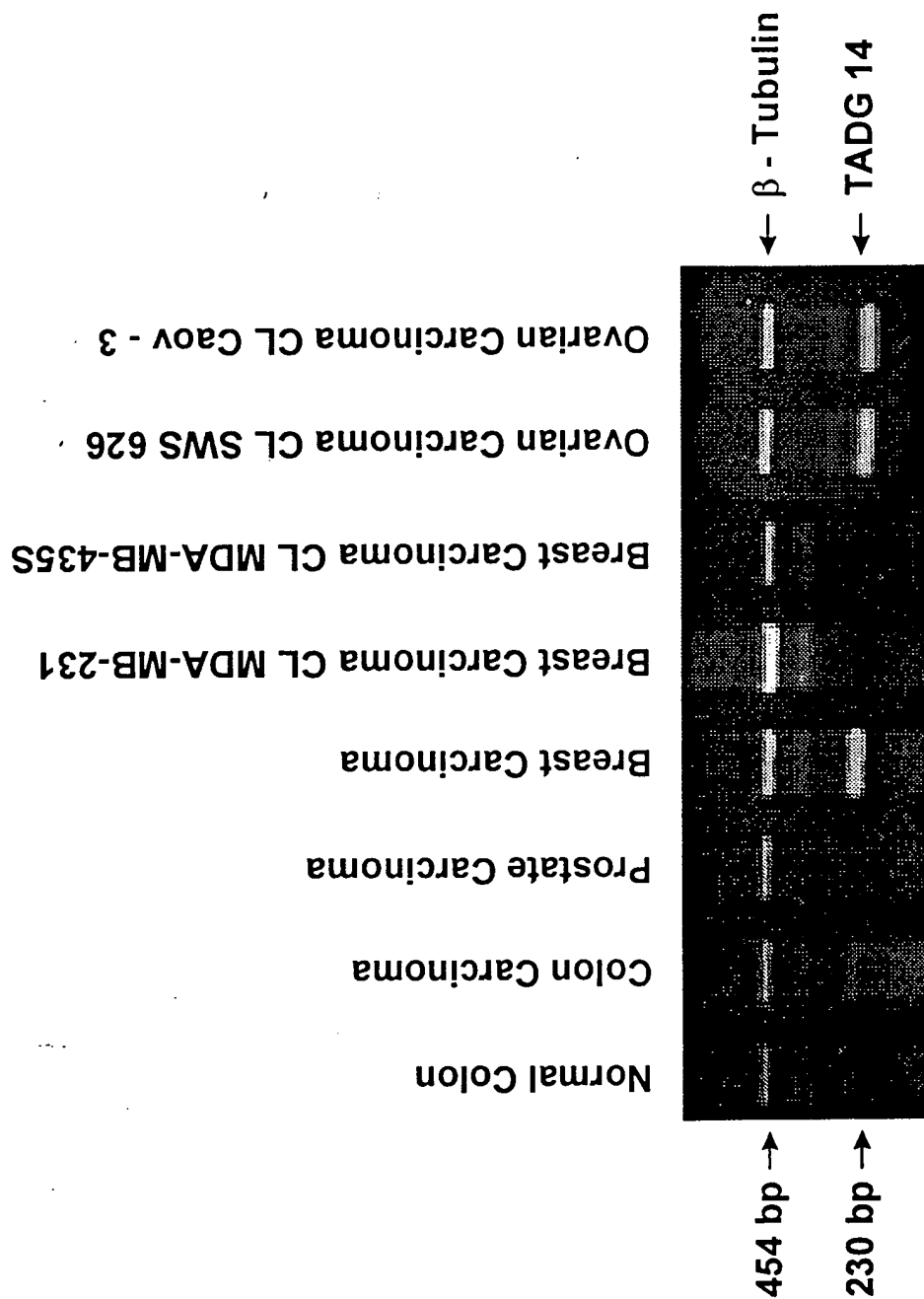


Figure 4. TADG-14 expression in tumors and cell lines.

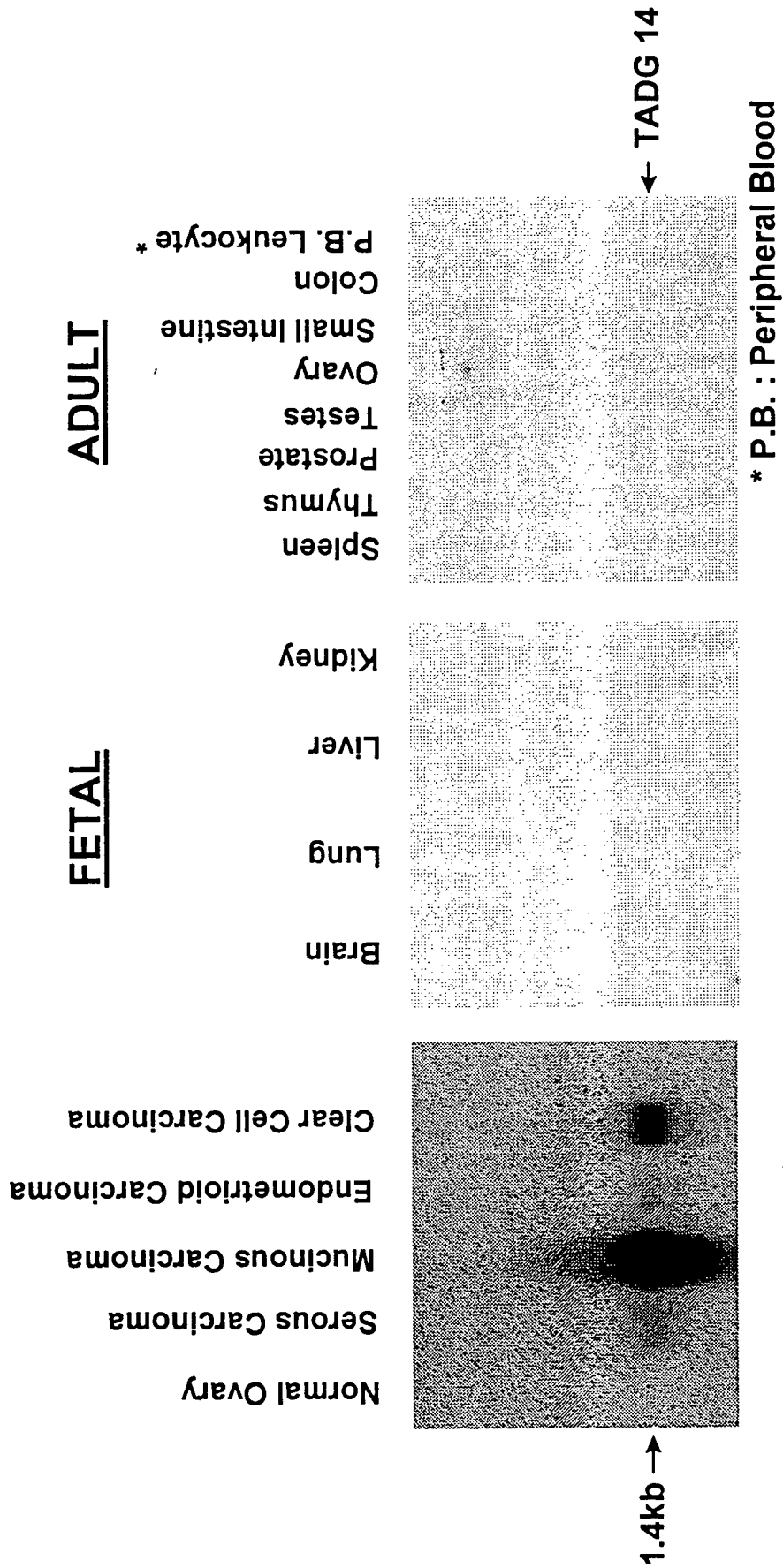


Figure 5. Blots: TADG-14 expression in fetal, adult and ovarian carcinoma tissues.

08915659 "082157"

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1  CTGTAGCAGGCAGAGCTTACCAAGTCTCTCCGAACTCAAATGGAAGAAATACCTTATGAA  60
61  TGTAAGAATGTAGGGGGTCATGGCTTGTAAATTTACACAGTGTAATGAAACCATCCTAGA  120
121 GGATTATGAGGAATCCTTTCTATGTGATTTTCAATCATAGCAAGCAAGAAAGGCTCCAGT  180
181 GTCAAGGTAGTTTCTTACAGGATATAAAACAGTCCATACTTGAGAGAAAAAACTTA  240
241 GATCTGAGTGATGGAATGTGAAGCAAATCTTTCAAATCAGTAGACATTTCTTGACATA  300
301 AAACACAGATGAGGAAAGGGCTTCAAATTAGAAGTTACGTAATCACCATCAGAAAGTTCA  360
361 TGTGTTGGTAAATTCTGTTACTAGAAATGTAGGAAATTCAGGTATAGCTTTGAATCCCAAT  420
421 TACACATTGGTCAGTGGGAAACTAAGGGCCTCCAACAGGCAAATTCAGGGAGGATAGGT  480
481 TTCAGGGAATGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGTGCGG  540
      M G R P R P R A A -
541 CCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCAC  600
      K T W M F L L L L G G A W A G H S R A Q -
601 AGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  660
      E D K V L G G H E C Q P H S Q P W Q A A -
661 CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGAGGTGGCAACTGGGTCC  720
      L F Q G Q Q L L C G G V L V G G N W V L -
721 TTACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTAC  780
      T A A H + C K K P K Y T V R L G D H S L Q -
781 AGAATAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCACACCCCTGCT  840
      N K D G P E Q E I P V V Q S I P H P C Y -
841 ACAACAGCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACC  900
      N S S D V E D H N H D + L M L L Q L R D Q -
901 AGGCATCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTG  960
      A S L G S K V K P I S L A D H C T Q P G -
961 GCCAGAAGTGACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCCGAGAGAATTTTCTTG  1020
      Q K C T V S G W G T V T S P R E N F P D -
1021 ACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACC  1080
      T L N C A E V K I F P Q K K C E D A Y P -
1081 CGGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCC  1140
      G Q I T D G M V C A G S S K G A D T C Q -
1141 AGGGCGATTCTGGAGGCCCTTGGTGTGTGATGGTGCATCCAGGGCATCACATCCTGGG  1200
      G D S + G G P L V C D G A L Q G I T S W G -
1201 GCTCAGACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACC  1260
      S D P C G R S D K P G V Y T N I C R Y L -
1261 TGGACTGGATCAAGAAGATCATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCT  1320
      D W I K K I I G S K G * SEQ ID NO: 7
1321 CCCTTAATAAACTACGGAATTC SEQ ID NO: 6

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 = Kozak's Consensus sequence

+ = Conserved amino acids of catalytic triad H, D, S

NSS = Possible N - linked glycosylation site

— = Poly - adenylation signal

 = Conserved nt of catalytic triad

○ = aa required for formation of an oxyanion hole for catalytic activity

FLLL = Secretion signal sequence

Figure 6. Complete sequence of TADG-14 transcript including ORF and common domains.

Figure 7. Homology of TADG-14 with mouse neuropsin. 76% identity for ORF. Low homology outside of ORF.

Percent Similarity: 76.471 Percent Identity: 76.471

Match display thresholds for the alignment(s):

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: = 5
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Neur.Nt x T14.Nt

May 7, 1997 08:33 ..

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Neur 477 AGAGGCCACCATGGGACGCCCCCACCCTGTGCAATCCAGCCGTGGATCC 526
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T14 506 AGACCTCACCATGGGACGCCCCGACCTCGTGCGGCCAAGACGTGGATGT 555

      .
527 TTCTGCTTCTGTTCATGGGAGCGTGGGCAGGGCTCACCAGAGCTCAGGGC 576
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
556 TCCTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGCACAGGAG 605

      .
577 TCCAAGATCCTGGAAGGTCGAGAGTGTATACCCCACTCCCAGCCTTGCCA 626
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
606 GACAAGGTGCTGGGGGTCATGAGTGCCAACCCATTTCGCAGCCTTGCCA 655

      .
627 GGCAGCCTTGTTCCAGGGCGAGAGACTGATCTGTGGGGGTGTCCTGGTTG 676
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
656 GCGGGCCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTGTAG 705

      .
677 GAGACAGATGGGTCTCTACGGCAGCCCACTGCAAAAAACAGAAGTACTCC 726
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
706 GTGGCAACTGGGTCTTACAGCTGCCCACTGTAAAAAACGAAATACACA 755

      .
727 GTGCGTCTGGGTGATCATAGCCTCCAGAGCAGAGATCAGCCGGAGCAGGA 776
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
756 GTACGCCTGGGAGACCACAGCCTACAGAATAAAGATGGCCCAGAGCAAGA 805

      .
777 GATCCAGGTGGCTCAGTCTATCCAGCATCCTTGCTACAACACAGCAACC 826
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
806 AATACCTGTGGTTCAGTCCATCCACACCCCTGCTACAACAGCAGCGATG 855

      .
827 CAGAAGATCACAGTCACGATATAATGCTCATTGCACTGCAGAACTCAGCA 876
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
856 TGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCA 905

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877 AACCTCGGGGACAAGGTGAAGCCGGTCCAACCTGGCCAATCTGTGTCCCAA 926
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
906 TCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCA 955

      .
927 AGTTGGCCAGAAGTGCATCATATCAGGCTGGGGCACTGTCACCAGCCCTC 976
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
956 GCCTGGCCAGAAGTGCACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCC 1005

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977 AAGAGAACTTTCCAAACACCCTCAACTGTGCGGAAGTGAAAATCTATTCC 1026
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1006 GAGAGAATTTTCTGACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCC 1055

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08915669-082197

1027 CAGAACAAGTGTGAGAGAGCCTATCCAGGGAAGATCACCGAGGGCATGGT 1076
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 1056 CAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGT 1105
 1077 CTGTGCTGGCAGCAGCAATGGAGCTGACACGTGCCAGGGTGACTCAGGAG 1126
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1106 CTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAG 1155
 1127 GCCCTCTGGTGTGCGACGGGATGCTCCAGGGCATCACCTCATGGGGCTCA 1176
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 1156 GCCCCCTGGTGTGTGATGGTGCACCTCCAGGGCATCACATCCTGGGGCTCA 1205
 1177 GACCCCTGTGGGAAACCCGAGAAACCTGGAGTCTACACCAAAATCTGCCG 1226
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1206 GACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCG 1255
 1227 CTACACTACCTGGATCAAGAAGACCATGGACAACAGGGACTGATCCTGG 1275
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08915659.082197

Percent Similarity: 77.220 Percent Identity: 72.201

Match display thresholds for the alignment(s):

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T14pro.Jack x Neur.Jack May 8, 1997 09:27 ..

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||||| | | . | . ||| ||||| . ||| | : | | | | | | | |
Neurop 1 MGRPPPCAIQPWILLLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAAL 50
51 FQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPV 100
||| : . : | | | | | | | | | | | | | | | | : | | | | |
51 FQGERLICGGVLVGDWRVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQV 100
101 VQSIPHPCYNSSDVEDHNDLMLLQLRDQASLGSKVKPISLADHCTQPGQ 150
||| ||||| . | . ||| . | : | : | . . | . | | | : | | . | |
101 AQSIQHPCYNNSPEDHSHDIMLIRLQNSANLGDVKVPVQLANLCPKVGQ 150
151 KCTVSGWGTVTSPRENFPTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
|| : | | | | | | | . | | | | | | | : | | | | | | . | : | | | | |
151 KCIISGWGTVTSPQENFPNTLNCAEVKIYSQNK CERAYPGKITEGMVCAG 200
201 SSKGADTCQGDSSGGLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLD 250
|| | | | | | | | | | | | | | | | : : | | | | | | | |
201 SSNGADTCQGDSSGGLVCDGMLQGITSWGS DPCGKPEKPGVYTKICRYTT 250
251 WIKKIIGSKG 260
||| | . . :
251 WIKKTMDNRD 260

Figure 8. Amino acid homology of TADG-14 with mouse neuropsin.

08915659.089157